

FIG. 1A-1

FIG. 1A-2

FIG. 1A

gtatttcata oooocagagag gctgcgogga ggcgcgcgcact ctgcactccctg gtggotggggo ctagggggcgc agagtcacgcgc cctgcactggc tgggggcggg cgcctccgagt cagcattggaa  
n e  
120  
agctctctccg gggctccttgt atttctctcg ctgcactgcag gactgcgcgt ccacggccgcgc agcggcttcc gtatgttgtt gggccatcag cagtattccg atcacatcag ggacacacac  
240  
s l c g u l u f l l l a r a g l p l q a r k r f r d u l g h e q y p d h n r e n h  
cattaccctg ccctgtcttc agatgaaat gatgggatg aacagctga tccagctgtg agcagcggag aggcacatg cagcactcc tggcagcag gccctgttga gccaccccta  
360  
q l r g u s s o e h e u o e q l y p v u r r g e g r u k d s u e g g a u q r a l  
accagtgatt caccggccctt gctgggttcc aatatacct tctagtga cctgtgttcc cccagatgcc agacggagaa tccacggc aatactct atagagagaa ctgcagact  
480  
t s o s p a l u g s h i t f u u h l u f p r c q k e d a h g h i u y e a m c a s  
gatttggac tggctttcga cccgtatgtc tacacttga ccacaggggc agacatcag gactggag acacacacag ccacggccag cactcaggt tcccgacgg gacgccttc  
600  
d l e l a s d p y u y n u t t g a d o e d u e d h t s q g q h l r f p d g k p f  
cctccccc accgacgga gatattgac ttctgtacg tcttcacac acttggtag tatttcara agctgggtca gtgttcagca cagatttcta taacacact caacttcaca  
720  
p r p h g a k k u h f u y u f h t l g q y f q k l g q c s a r u s i h t u h l t  
gttggccctc agctatcga agtattgtc tttcagagc accggccggc atacattccc atctccaaag tgaacacgt gtatgtata acacatcaga tccctatatt cgtacacatg  
840  
u g p q u n e u i u f a r h g a r a y i p i s k u k d u y u i t o q i p i f u t n  
tacacagaa atacccgga ctctctgat gaaccttcc tcaagacct cccattttc ttcatgttcc tcatcaga tccacgtcat ttctcact actctgccat ttcttcaag  
960  
y q k h d r h s s o e t f l r d l p i f f d u l i h d p s h f l h y s a i s y k

FIG. 1A-1

09943075 : 041002

TGGACCTTGG GGGACACAC TGGCCCTGTTT GTCTCCACA ATCACACTTT GATACACAG TATGTGCTCA ATGACACCTT CACCTTTAAC CTCACCGTGC AACCTGCAGT GCCCGGACCA 1080  
 U H F G D H T G L F U S H H H T L H H T Y U L H H T F H F H L T U Q T A U P G P  
 TGGCCCTCAC CACACCTTC GCCCTCTCT TCGACTCTC CTTCGCCCT CTTCGCCCT TATCACACAT TATCACACAT TATGCTCTCT TATGCTCTCT TATGCTCTCT TATGCTCTCT TATGCTCTCT 1200  
 C P S P T P S S S T S P S P A S S P S P T L S T P S P S L H P T G Y K S H E  
 CTGAGTGACA TTTCATGCA AACTGCGCA ATATACACAT ATGCTTACT CAGAGCCACC ATCACATTTG TAGATGGAT CCAAGAGTC AACATCATCC AGGTAGCAGA TGTCCTATC 1320  
 L S D I S H E H C A I H R Y G Y F A A T I T I U D G I L E U H I I Q U A D U P I  
 CCCACACTGC AGCTTACCA CTCACCTGAT GACTTCTATG TGACCTGCA AGGGGCCACT CCCACGGAG CCTGTACCAT CATCTCTGAC CCCACCTGCC AGATGCCCCA GACAGGGTG 1440  
 P T L Q P D H S L H D F I U T C K G A T P T E A C T I I S D P T C Q I A Q H R U  
 TGCACCCCGG TGGCTGTGGA TGACCTGTGC CTCCCTGTCG TGAGGAGAGC CTTCATATGG TCCGGACAGT ACCTGTGGA TTTCACCTCTG GAGAGCGATG CAGCCCTGCC CCTACCCAGC 1560  
 C S P U A U D E L C L L S U A R A F H G S G T Y C U H F T L G D D A S L A L T S  
 GGGCTGATCT CTATCCCTGG CAGAGACCTA GGGCTCCCTC TGAGACACAT GATGGTCTC CTGATCTCCA TTGGCTGCCCT GGGCTATGTT GTACCATGG TTACCATCTT GCTGTACAA 1680  
 A L I S I P G K D L G S P L A T U H G U L I S I G C L A H F U T H U T I L L Y K  
 AACACACAGA CGTACACGCC ATATGGAAC TGCACCCAGA ACGTGTGCA GGGCAAGGC CTGAGTGTIT TTCTACGCA TGAAGAGCC CCGTCTCTCC GAGAGAGCC GAGAGAGGAT 1800  
 K H K T Y K P I G H C T R H U U K G K G L S U F L S H A K A P F S R G D R E K D  
 CACCTGCTCC AGGACACGCC ATGATGCTC TATGCTCTC CTTCTCTC TGGCTGCTC TGGCTGCTC TGGCTGCTC TGGCTGCTC TGGCTGCTC TGGCTGCTC TGGCTGCTC TGGCTGCTC 1920  
 P L L Q D K P U N L  
 TCTACGGATT ATTGTAAGG GTATGCTATG GTTGGGGG GTGTTGAT GTGCTGCTG GTGCTGCTG GTGCTGCTG GTGCTGCTG GTGCTGCTG GTGCTGCTG GTGCTGCTG GTGCTGCTG 2040  
 GGGGTGGGCA CATTGCTCT GGGGGGGGG GTGCTGCTG GTGCTGCTG GTGCTGCTG GTGCTGCTG GTGCTGCTG GTGCTGCTG GTGCTGCTG GTGCTGCTG GTGCTGCTG GTGCTGCTG 2160  
 GTGCTGCTG GTGCTGCTG GTGCTGCTG GTGCTGCTG GTGCTGCTG GTGCTGCTG GTGCTGCTG GTGCTGCTG GTGCTGCTG GTGCTGCTG GTGCTGCTG GTGCTGCTG 2280  
 GTGCTGCTG GTGCTGCTG GTGCTGCTG GTGCTGCTG GTGCTGCTG GTGCTGCTG GTGCTGCTG GTGCTGCTG GTGCTGCTG GTGCTGCTG GTGCTGCTG GTGCTGCTG 2320

FIG. 1A-2

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EXON	BAC Start	BAC Stop	cDNA Start	cDNA Stop	Exon Length
1	83294	83455	1	162	162
2	89834	89986	163	314	152
3	90696	90839	315	458	144
4	93419	93594	459	634	176
5	96509	96665	635	791	157
6	96983	97300	792	1109	318
7	103044	103142	1110	1208	99
8	104413	104515	1209	1311	103
9	106494	106702	1312	1520	209
10	110048	110141	1521	1614	94
11	110592	111633	1615	2656	1042

poly A signal is position 111614-111619

translation start (ATG) is:  
cDNA: 92  
Gene: 83385

FIG. 1B

K-D

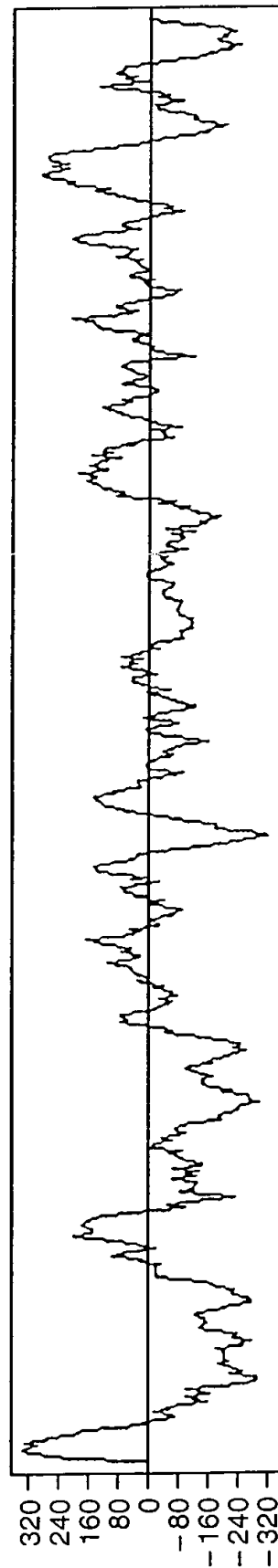


FIG. 1C

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FIG. 2A-1
FIG. 2A-2
FIG. 2A-3
FIG. 2A-4
FIG. 2A-5

FIG. 2A



rat	GTGTTCCCCA	GATGCCAGAA	GGAAGATGCC	AACGGCAATA	TCGTCTATGA	GAGGAACTGC	AGAAGTGATT	TGGAG	375
mouse	GTGTTCCCCA	GATGCCAGAA	GGAAGATGCT	AATGGCAATA	TCGTCTATGA	GAAGAACTGC	AGGAATGATT	TGGGA	375
human	ATATTCCCTA	GATGCCAATA	GGAAGATGCC	AATGGCAACA	TAGTCTATGA	GAAGAACTGC	AGAAATGAGG	CTGGT	375
rat	CTGGCTTCTG	ACCCGTATGT	CTACAACTGG	ACCACAGGGG	CAGACGATGA	GGACTGGGAA	GACAACACCA	GCCAA	450
mouse	CTGACATCTG	ACCTGCATGT	CTACAACTGG	ACTGCAGGGG	CAGATGATGG	TGACTGGGAA	GATGGCACCA	GCCGA	450
human	TTATCTGCTG	ATCCATATGT	TTACAACTGG	ACAGCATGGT	CAGAGGACAG	TGACGGGGAA	AATGGCACCG	GCCAA	450
rat	GGCCAGCAC	TCAGGTTCCC	CGACGGGAAG	CCCTTCCCTC	GCCCCACCG	ACGGAAGAA	TGGAACCTCG	TCTAC	525
mouse	AGCCAGCATC	TCAGGTTCCC	GGACAGGAGG	CCCTTCCCTC	GCCCCACATGG	ATGGAAGAA	TGGAGCTTTG	TCTAC	525
human	AGCCATCATA	ACGTCTTCCC	TGATGGGAAA	CCTTTTCCTC	ACCACCCCGG	ATGGAGAAGA	TGGAATTCA	TCTAC	525
rat	GTCTTCCACA	CACCTTGGTCA	GTATTTTCAA	AAGCTGGGTC	AGTGTTTCAGC	ACGAGTTTCT	ATAAACACAG	TCAAC	600
mouse	GTCTTTCACA	CACCTTGGCCA	GTATTTGCCA	AAACTGGGTC	GGTGTTTCAGC	ACGGGTTTCT	ATAAACACAG	TCAAC	600
human	GTCTTCCACA	CACCTTGGTCA	GTATTTCCAG	AAATTGGGAC	GATGTTTCAGT	GAGAGTTTCT	GTGAACACAG	CCAAT	600
rat	TTGACAGTTG	GCCCTCAGGT	CATGGAAGTG	ATTGTCTTTC	GAAGACACGG	CCGGGCATAC	ATTCCCATCT	CCAAA	675
mouse	TTGACAGCTG	GCCCTCAGGT	CATGGAAGTG	ACTGTCTTTC	GAAGATACGG	CCGGGCATAC	ATTCCCATCT	CGAAG	675
human	GTGACACTTG	GGCCTCAACT	CATGGAAGTG	ACTGTCTTACA	GAAGACATGG	ACGGGCATAT	GTTCCCATCG	CACAA	675

FIG. 2A-2

rat	GTGAAAGACG	TGTATGTGAT	AACAGATCAG	ATCCCTATAT	TCGTGACCAT	GTACCAGAAG	AATGACCGGA	ACTCG	750
mouse	GTGAAAGATG	TGTATGTGAT	AACAGATCAG	ATCCCTGTAT	TCGTGACCAT	GTCCCAGAAG	AATGACAGGA	ACTTG	750
human	GTGAAAGATG	TGTACGTGGT	AACAGATCAG	ATTCCTGTGT	TTGTGACTAT	GTTCCAGAAG	AACGATCGAA	ATTCA	750
rat	TCTGATGAAA	CCTTCCTCAG	AGACCTCCCC	ATTTCTTCG	ATGTCCTCAT	TCACGATCCC	AGTCATTTC	TCAAC	825
mouse	TCTGATGAGA	TCTTCCTCAG	AGACCTCCCC	ATCGTCTTCG	ATGTCCTCAT	TCATGATCCC	AGCCACTTC	TCAAC	825
human	TCCGACGAAA	CCTTCCTCAA	AGATCTCCCC	ATTATGTTG	ATGTCCTGAT	TCATGATCCT	AGCCACTTC	TCAAT	825
rat	TACTCTGCCA	TTTCCTACAA	GTGGAACCTT	GGGACAACA	CTGGCCTGTT	TGTCTCCAAC	AATCACACTT	TGAAT	900
mouse	GACTCTGCCA	TTTCCTACAA	GTGGAACCTT	GGGACAACA	CTGGCCTGTT	TGTCTCCAAC	AATCACACTT	TGAAT	900
human	TATTCTACCA	TTAACTACAA	GTGGAGCTTC	GGGATAATA	CTGGCCTGTT	TGTTTCCACC	AATCATACTG	TGAAT	900
rat	CACACGTATG	TGCTCAATGG	AACCTTCAAC	TTTAACTCA	CCGTGCAAC	TGCAGTGCCG	GG-----	-ACCA	966
mouse	CACACTTATG	TGCTCAATGG	AACCTTCAAC	CTTAACTCA	CCGTGCAAC	TGCAGTGCCC	GG-----	-GCCA	966
human	CACACGTATG	TGCTCAATGG	AACCTTCAGC	CTTAACTCA	CTGTGAAAGC	TGCAGCACCA	GGACCTTGTC	CGCCA	975
rat	-TGCC-CC-T	CACCCACACC	TTGCGCTTCT	TCTTCGACTT	CTCCTTC---	---GCCTGCA	TCTTCGCTT	CA---	1029
mouse	-TGCC-C--T	--CCC--T	TTGCGCTTCG	ACTCGCCTT	CACCTTCAAC	TCCGCGCCTTA	CCTTCGCTT	CACCT	1032
human	CCGCCACCCAC	CACCCAGACC	TTC-----	-----AA-	-----A	-----	-----	-ACC-	1004

FIG. 2A-3







FIG. 2B-1
FIG. 2B-2

FIG. 2B

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rat	MESLCGVLVF	LLLAAGLPLQ	AAKRRDVLG	HEQYPDHMR	NNQLRGWSSD	50
mouse	MESLCGVLGF	LLLAAGLPLQ	AAKRRDVLG	HEQYPDHMR	HNQLRGWSSD	50
human	MECLYYFLGF	LLLAARLPLD	AAKRFHDVLG	NERPSAYMR	HNQLNGWSSD	50
rat	ENEWDEQLYP	VWRRGGRWK	DSWEGGRVQA	ALTSDSPALV	GSNITFVVNL	100
mouse	ENEWDEHLYP	VWRRGDGRWK	DSWEGGRVQA	VLTSDSPALV	GSNITFVVNL	100
human	ENDWNEKLYP	VWKRGDMRWK	NSWKGGRVQA	VLTSDSPALV	GSNITFAVNL	100
rat	VFPRCQKEDA	NGNIVYERN	RSDLELASDP	YVYNWTTGAD	DEDWEDNTSQ	150
mouse	VFPRCQKEDA	NGNIVYEKNC	RNDLGLTSDL	HVYNWTTAGAD	DGDWEDGTSR	150
human	IFPRCQKEDA	NGNIVYEKNC	RNEAGLSADP	YVYNWTTAWSE	DSDGENGTTGQ	150
rat	GQHLRFDPDGK	PFPRPHGRKK	WNFVYVFHTL	GQYFQKLGQC	SARVSINTVN	200
mouse	SQHLRFDPDRR	PFPRPHGWKK	WSFVYVFHTL	GQYFQKLGRC	SARVSINTVN	200
human	SHHNVFPDGK	PFPHHPGWR	WNFIYVFHTL	GQYFQKLGRC	SVRVSNTAN	200
rat	LTVGPQVMEV	IVFRRHGRAY	IPISKVKDVY	VITDQIPIFV	TMYQKNDRNS	250
mouse	LTAGPQVMEV	TVFRRYGRAY	IPISKVKDVY	VITDQIPIFV	TMSQKNDRNL	250
human	VTLPQQLMEV	TVYRRHGRAY	VPIAQVKDVY	VVTDQIPIFV	TMFQKNDRNS	250
rat	SDETFLRDL	IFFDVLIHDP	SHFLNYS AIS	YKWNFGDNTG	LFVSNHHTLN	300
mouse	SDEIFLRDL	IVFDVLIHDP	SHFLNDS AIS	YKWNFGDNTG	LFVSNHHTLN	300
human	SDETFLKDL	IMFDVLIHDP	SHFLNYSTIN	YKWSFGDNTG	LFVSTNHTVN	300

FIG. 2B-1

rat	HTYVLNGTFN	FNLTVQTAVP	GPCSPTPS-	-PSSSTSPSP	ASSPSPTLST	348
mouse	HTYVLNGTFN	LNLTVQTAVP	GPCPPSPST	PPSPSTPPLP	SPSPLPTLST	350
human	HTYVLNGTFS	LNLTVKAAP	GPCPPPPP--	-----PPRP	-----SK	334
rat	PSPSLMPTGY	KSMELSDISN	ENCRINRYGY	FRATITIVDG	ILEVNI IQVA	398
mouse	PSPSLMPTGY	KSMELSDISN	ENCRINRYGY	FRATITIVEG	ILEVSIMQIA	400
human	PTPSLGPAGD	NPLELSRIPD	ENCQINRYGH	FQATITIVEG	ILEVNI IQMT	384
rat	DVPIPTLQPD	NSLMDFIVTC	KGATPTEACT	IISDPTCQIA	QNRVCSPVAV	448
mouse	DVPMPTPQPA	NSLMDFTVTC	KGATPMEACT	IISDPTCQIA	QNRVCSPVAV	450
human	DVLMPPVPWE	SSLIDFVVTC	QGSIPTEVCT	IISDPTCEIT	QNTVCSPVDV	434
rat	DELCLLSVRR	AFNGSGTYCV	NFTLGDDASL	ALTSALISIP	GKDLGSPLRT	498
mouse	DGLCLLSVRR	AFNGSGTYCV	NFTLGDDASL	ALTSTLISIP	GKDPDSPLRA	500
human	DEMCLLTVRR	TFNGSGTYCV	NFTLGDDTSL	ALTSTLISVP	DRDPASPLRM	484
rat	VNGVLISIGC	LAMEVTMVTI	LLYKKHKTYK	PIGNCTRNVV	KGKGLSVFSL	548
mouse	VNGVLISIGC	LAVLVTMVTI	LLYKKHKAYK	PIGNCPRNTV	KGKGLSVLLS	550
human	ANSALISVGC	LAIFVTVISL	LVYKKHKEYN	PIENSPGNVV	RSKGLSVFLN	534
rat	HAKAPFSRGD	REKDPLLQDK	PW--ML	572		
mouse	HAKAPFFRGD	QEKDPLLQDK	PR--TL	574		
human	RAKAVFFPGN	QEKDPLLKNQ	EFKGVS	560		

FIG. 2B-2

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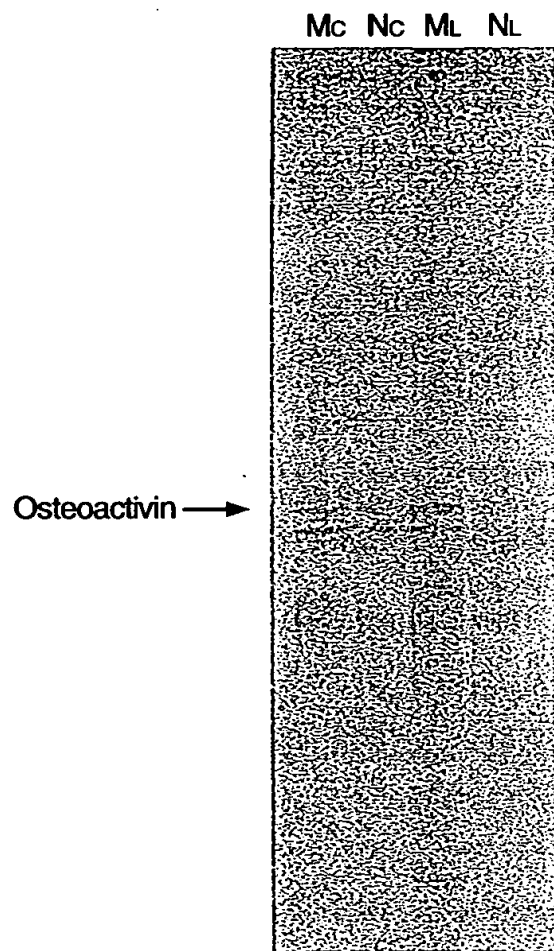


FIG. 3

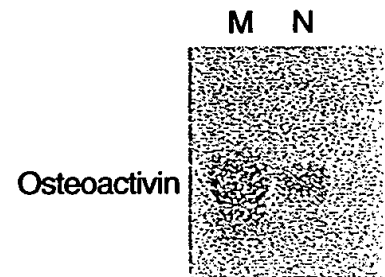


FIG. 4A

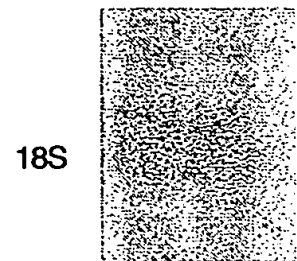


FIG. 4B

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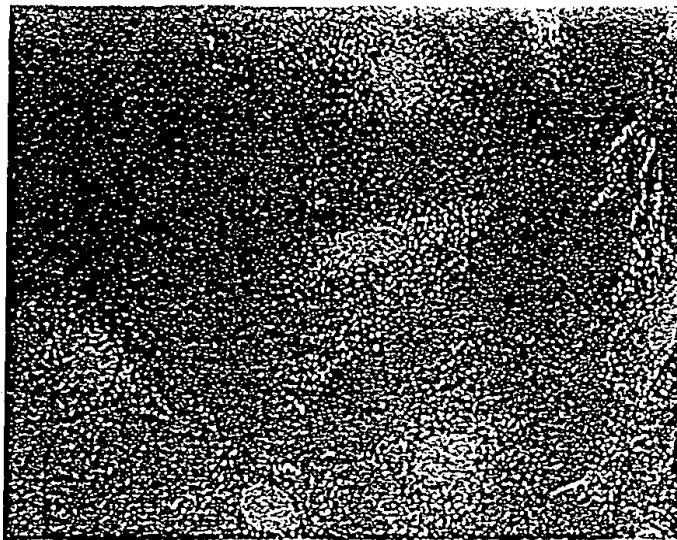


FIG. 5

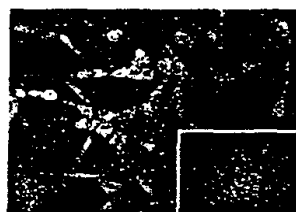


FIG. 5A

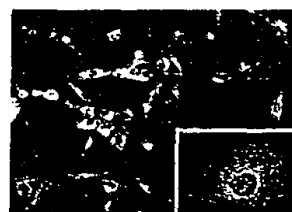


FIG. 5B



FIG. 5C

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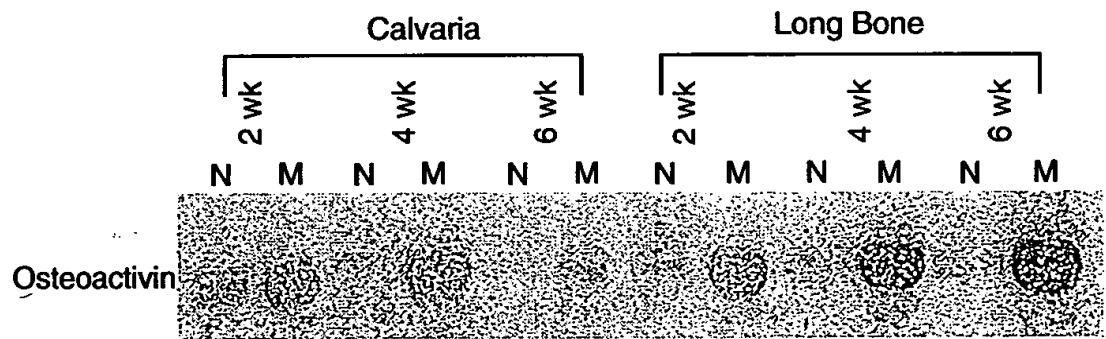


FIG. 6

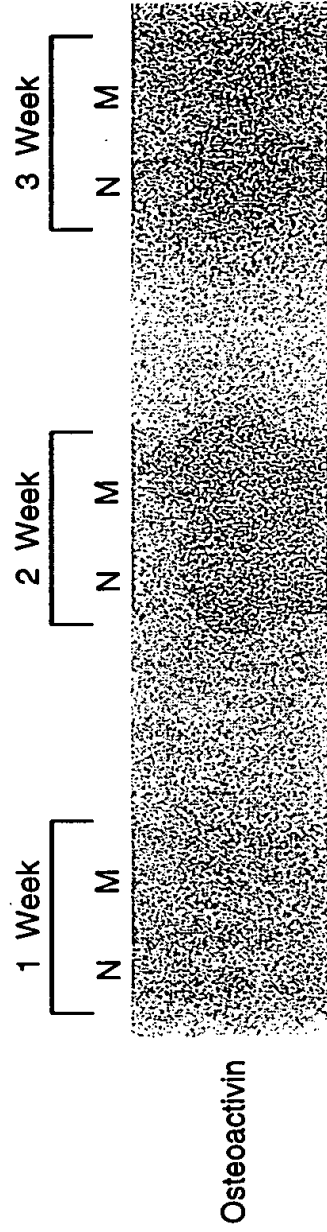


FIG. 7A

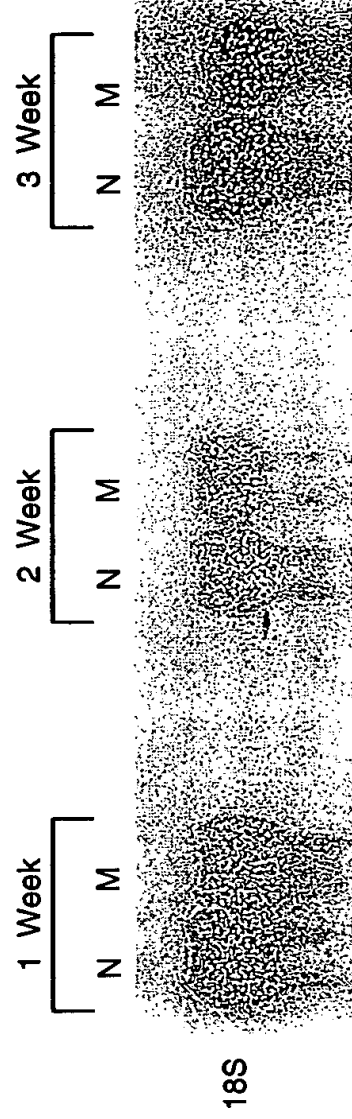


FIG. 7B

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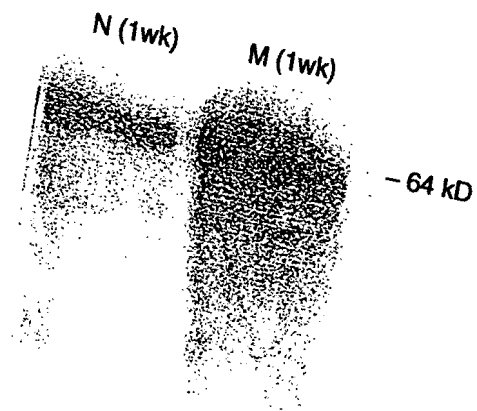


FIG. 8



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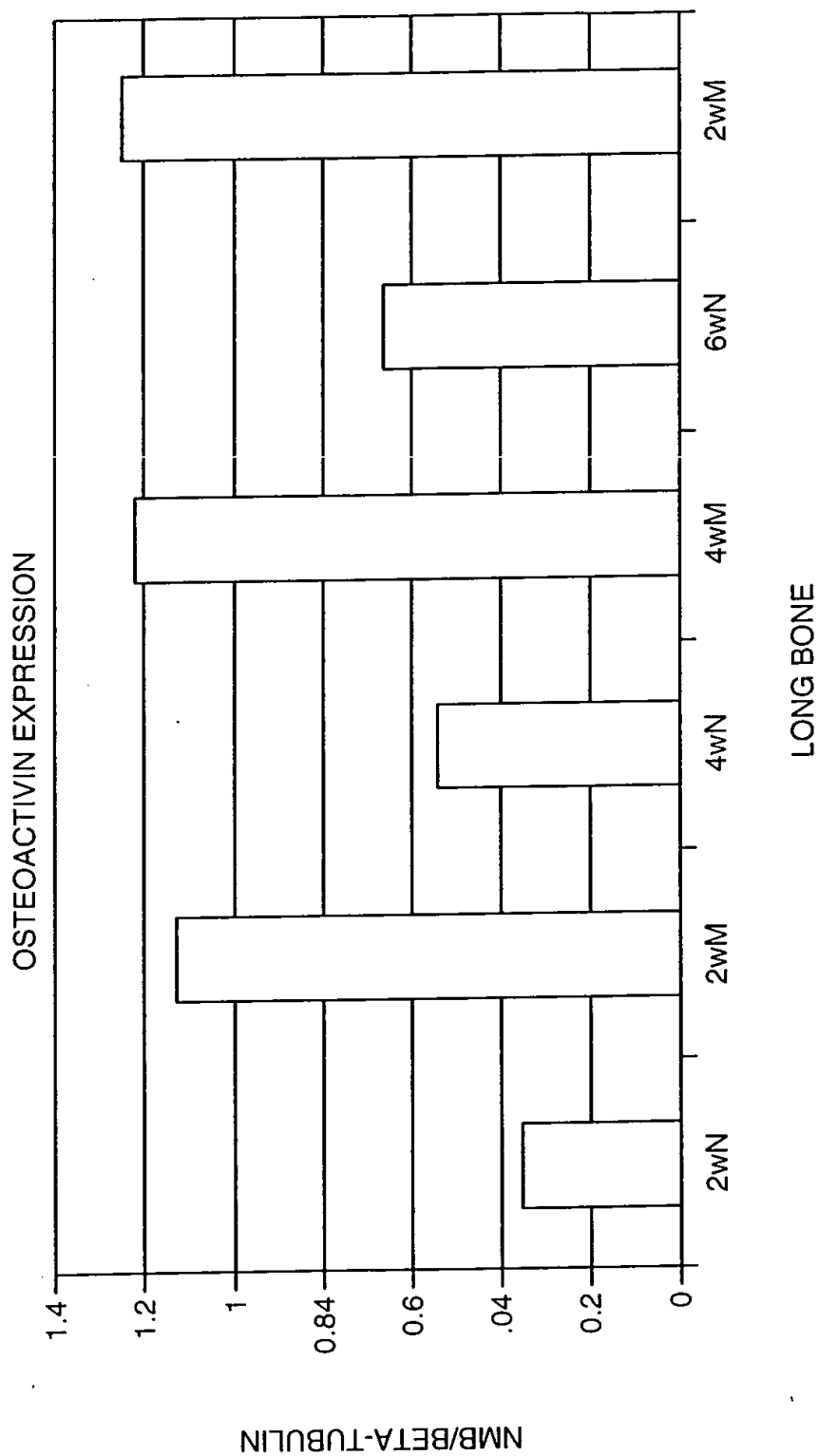


FIG. 9

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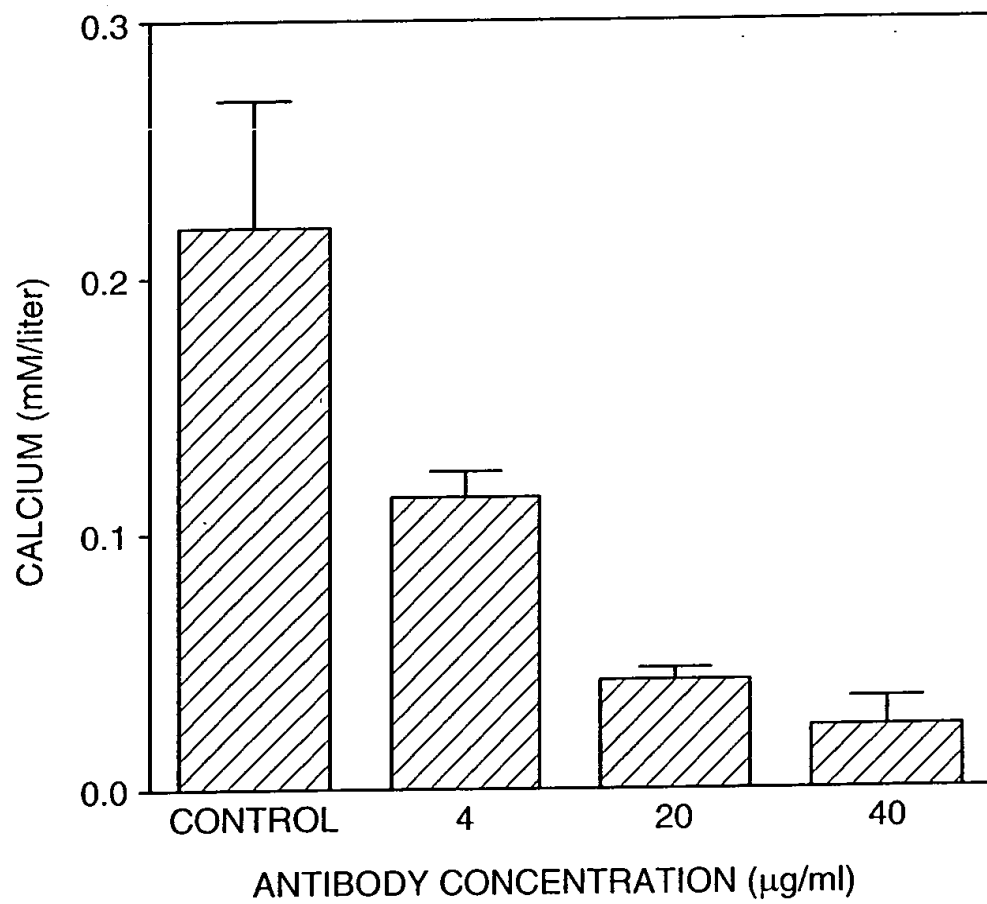


FIG. 10